Supplemental Data

Supplemental Table I. MS and DMS settings for phospholipid and sphingolipid analysis.

Phospholipid/Sphingolipid	Scan[1]	Mode[1]	COV[2]	Mode[2]
Phosphatidylcholine	PIS 184.1	POS	0.3	POS
Phosphatidylethanolamine	NL 141.1	POS	-4.0	NEG
Phosphatidylserine	NL 185.1	POS	2.7	POS
Phosphatidylinositol	PIS 241.2	NEG	3.0	NEG
Phosphatidylglycerol	NL 172.1	POS	-2.8	NEG
Phosphatidic Acid	NL 98.0	POS	-2.9	NEG
Lyso Phosphatidylcholine	PIS 184.1	POS	-8.5	POS
Lyso Phosphatidylethanolamine	NL 141.1	POS	-13.3	NEG
Lyso Phosphatidylserine	NL 185.1	POS	-1.6	NEG
Lyso Phosphatidylinositol	PIS 241.2	NEG	1.8	NEG
Lyso Phosphatidylglycerol	NL 172.1	POS	-7.4	NEG
Lyso Phosphatidic Acid	NL 98.0	POS	-14.4	NEG
Sphingomylein	PIS 184.1	POS	2.5	POS
Ceramide	PIS 264.2	POS	-5.0	POS

[1] Multiplex MS settings: precursor ion scan (PIS) or neutral loss scan (NL) with ionization mode set to either positive (POS) or negative (NEG)

[2] EMS scan settings for DMS: compensation voltage (COV) in V with ionization mode set to either positive (POS) or negative (NEG)

Supplemental Figure I. Lipid profiles recorded with HILIC alone and with HILIC combined with DMS. Left panel shows HILIC-based chromatographic separation of lipids extracted from human serum using PIS and NL scans in either positive (+) or negative (-) ion mode without DMS. Right panels show EMS scans in either positive (+) or negative mode with DMS. Selected COV values were specific for each phospholipid class.